

23546-08072/US (BIOLO002US)
SEQUENCE LISTING

<110> George Tachas
Kenneth W. Dobie
Ravi Jain
Christopher Ian Belyea
Mark Andrew Heffernan

<120> MODULATION OF GROWTH HORMONE RECEPTOR EXPRESSION AND INSULIN LIKE
GROWTH FACTOR EXPRESSION

<130> BIOLO002US

<150> 60/451,455

<151> 2003-02-28

<160> 268

<210> 1
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 1
tccgtcatcg ctcctcaggg

20

<210> 2
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

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<223> Antisense Oligonucleotide

<400> 2

gtgcgcgcga gccccaaaatc

20

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 3

atgcattctg cccccaaggaa

20

<210> 4

<211> 4414

<212> DNA

<213> H. sapiens

<220>

<220>

<221> CDS

<222> (44) ... (1960)

<400> 4

ccgcgcgtctc tgatcagagg cgaagctcg aggtcctaca ggt atg gat ctc tgg

55

Met Asp Leu Trp

1

cag ctg ctg ttg acc ttg gca ctg gca gga tca agt gat gct ttt tct
Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser Asp Ala Phe Ser

103

5

10

15

20

gga agt gag gcc aca gca gct atc ctt agc aga gca ccc tgg agt ctg	25	30	35	151
Gly Ser Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu				
caa agt gtt aat cca ggc cta aag aca aat tct tct aag gag cct aaa	40	45	50	199
Gln Ser Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys				
ttc acc aag tgc cgt tca cct gag cga gag act ttt tca tgc cac tgg	55	60	65	247
Phe Thr Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp				
aca gat gag gtt cat cat ggt aca aag aac cta gga ccc ata cag ctg	70	75	80	295
Thr Asp Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu				
ttc tat acc aga agg aac act caa gaa tgg act caa gaa tgg aaa gaa	85	90	95	343
Phe Tyr Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu				
tgc cct gat tat gtt tct gct ggg gaa aac agc tgt tac ttt aat tca	105	110	115	391
Cys Pro Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser				
tcg ttt acc tcc atc tgg ata cct tat tgt atc aag cta act agc aat	120	125	130	439
Ser Phe Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn				
ggt ggt aca gtg gat gaa aag tgt ttc tct gtt gat gaa ata gtg caa	135	140	145	487
Gly Gly Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln				
cca gat cca ccc att gcc ctc aac tgg act tta ctg aac gtc agt tta	150	155	160	535
Pro Asp Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu				
act ggg att cat gca gat atc caa gtg aga tgg gaa gca cca cgc aat				583
Thr Gly Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn				

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165

170

175

180

gca gat att cag aaa gga tgg atg gtt ctg gag tat gaa ctt caa tac 631
 Ala Asp Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr
 185 190 195

aaa gaa gta aat gaa act aaa tgg aaa atg atg gac cct ata ttg aca 679
 Lys Glu Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr
 200 205 210

aca tca gtt cca gtg tac tca ttg aaa gtg gat aag gaa tat gaa gtg 727
 Thr Ser Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val
 215 220 225

cgt gtg aga tcc aaa caa cga aac tct gga aat tat ggc gag ttc agt 775
 Arg Val Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser
 230 235 240

gag gtg ctc tat gta aca ctt cct cag atg agc caa ttt aca tgt gaa 823
 Glu Val Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu
 245 250 255 260

gaa gat ttc tac ttt cca tgg ctc tta att att atc ttt gga ata ttt 871
 Glu Asp Phe Tyr Phe Pro Trp Leu Leu Ile Ile Ile Phe Gly Ile Phe
 265 270 275

ggg cta aca gtg atg cta ttt gta ttc tta ttt tct aaa cag caa agg 919
 Gly Leu Thr Val Met Leu Phe Val Phe Leu Phe Ser Lys Gln Gln Arg
 280 285 290

att aaa atg ctg att ctg ccc cca gtt cca gtt cca aag att aaa gga 967
 Ile Lys Met Leu Ile Leu Pro Pro Val Pro Val Pro Lys Ile Lys Gly
 295 300 305

atc gat cca gat ctc ctc aag gaa gga aaa tta gag gag gtg aac aca 1015
 Ile Asp Pro Asp Leu Leu Lys Glu Gly Lys Leu Glu Glu Val Asn Thr
 310 315 320

atc tta gcc att cat gat agc tat aaa ccc gaa ttc cac agt gat gac 1063

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Ile Leu Ala Ile His Asp Ser Tyr Lys Pro Glu Phe His Ser Asp Asp
 325 330 335 340

tct tgg gtt gaa ttt att gag cta gat att gat gag cca gat gaa aag 1111
 Ser Trp Val Glu Phe Ile Glu Leu Asp Ile Asp Glu Pro Asp Glu Lys
 345 350 355

act gag gaa tca gac aca gac aga ctt cta agc agt gac cat gag aaa 1159
 Thr Glu Glu Ser Asp Thr Asp Arg Leu Leu Ser Ser Asp His Glu Lys
 360 365 370

tca cat agt aac cta ggg gtg aag gat ggc gac tct gga cgt acc agc 1207
 Ser His Ser Asn Leu Gly Val Lys Asp Gly Asp Ser Gly Arg Thr Ser
 375 380 385

tgt tgt gaa cct gac att ctg gag act gat ttc aat gcc aat gac ata 1255
 Cys Cys Glu Pro Asp Ile Leu Glu Thr Asp Phe Asn Ala Asn Asp Ile
 390 395 400

cat gag ggt acc tca gag gtt gct cag cca cag agg tta aaa ggg gaa 1303
 His Glu Gly Thr Ser Glu Val Ala Gln Pro Gln Arg Leu Lys Gly Glu
 405 410 415 420

gca gat ctc tta tgc ctt gac cag aag aat caa aat aac tca cct tat 1351
 Ala Asp Leu Leu Cys Leu Asp Gln Lys Asn Gln Asn Asn Ser Pro Tyr
 425 430 435

cat gat gct tgc cct gct act cag cag ccc agt gtt atc caa gca gag 1399
 His Asp Ala Cys Pro Ala Thr Gln Gln Pro Ser Val Ile Gln Ala Glu
 440 445 450

aaa aac aaa cca caa cca ctt cct act gaa gga gct gag tca act cac 1447
 Lys Asn Lys Pro Gln Pro Leu Pro Thr Glu Gly Ala Glu Ser Thr His
 455 460 465

caa gct gcc cat att cag cta agc aat cca agt tca ctg tca aac atc 1495
 Gln Ala Ala His Ile Gln Leu Ser Asn Pro Ser Ser Leu Ser Asn Ile
 470 475 480

23546-08072/US (BIOLO002US)

gac ttt tat gcc cag gtg agc gac att aca cca gca ggt agt gtg gtc	1543		
Asp Phe Tyr Ala Gln Val Ser Asp Ile Thr Pro Ala Gly Ser Val Val			
485	490	495	500
ctt tcc ccg ggc caa aag aat aag gca ggg atg tcc caa tgt gac atg	1591		
Leu Ser Pro Gly Gln Lys Asn Lys Ala Gly Met Ser Gln Cys Asp Met			
505	510	515	
cac ccg gaa atg gtc tca ctc tgc caa gaa aac ttc ctt atg gac aat	1639		
His Pro Glu Met Val Ser Leu Cys Gln Glu Asn Phe Leu Met Asp Asn			
520	525	530	
gcc tac ttc tgt gag gca gat gcc aaa aag tgc atc cct gtg gct cct	1687		
Ala Tyr Phe Cys Glu Ala Asp Ala Lys Lys Cys Ile Pro Val Ala Pro			
535	540	545	
cac atc aag gtt gaa tca cac ata cag cca agc tta aac caa gag gac	1735		
His Ile Lys Val Glu Ser His Ile Gln Pro Ser Leu Asn Gln Glu Asp			
550	555	560	
att tac atc acc aca gaa agc ctt acc act gct gct ggg agg cct ggg	1783		
Ile Tyr Ile Thr Thr Glu Ser Leu Thr Thr Ala Ala Gly Arg Pro Gly			
565	570	575	580
aca gga gaa cat gtt cca ggt tct gag atg cct gtc cca gac tat acc	1831		
Thr Gly Glu His Val Pro Gly Ser Glu Met Pro Val Pro Asp Tyr Thr			
585	590	595	
tcc att cat ata gta cag tcc cca cag ggc ctc ata ctc aat gcg act	1879		
Ser Ile His Ile Val Gln Ser Pro Gln Gly Leu Ile Leu Asn Ala Thr			
600	605	610	
gcc ttg ccc ttg cct gac aaa gag ttt ctc tca tca tgt ggc tat gtg	1927		
Ala Leu Pro Leu Pro Asp Lys Glu Phe Leu Ser Ser Cys Gly Tyr Val			
615	620	625	
agc aca gac caa ctg aac aaa atc atg cct tag cttttttttt gtttcccaag	1980		
Ser Thr Asp Gln Leu Asn Lys Ile Met Pro			
630	635		

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agctacgtat ttaatagcaa agaattgact gggcaataa cgtttaagcc aaaacaatgt 2040
ttaaacctt tttgggggag tgacaggatg gggtatggat tctaaaatgc cttttcccaa 2100
aatgttggaa tatgtatgtt aaaaaataag aagaatgctt aatcagatag atattcctat 2160
tgtgcaatgt aaatattttt aagaattgtg tcagactgtt tagtagcagt gattgtctta 2220
atattgtggg tgttaatttt tgatactaag cattgaatgg ctatgtttt aatgtatagt 2280
aaatcacgct tttgaaaaaa gcgaaaaaat caggtggctt ttgcggttca ggaaaattga 2340
atgcaaacca tagcacaggc taatttttg ttgtttctta aataagaaac ttttttattt 2400
aaaaaaactaa aaactagagg tgagaaattt aaactataag caagaaggca aaaatagtt 2460
ggatatgtaa aacatttact ttgacataaa gttgataaag attttttaat aatttagact 2520
tcaagcatgg ctatttata ttacactaca cactgtgtac tgcagttggc atgacccctc 2580
taaggagtgt agcaactaca gtctaaagct ggttaatgt tttggccaat gcacctaaag 2640
aaaaacaaac tcgttttta caaagccctt ttataccctcc ccagactcct tcaacaattc 2700
taaaatgatt gtagtaatct gcattattgg aatataattg ttttatctga atttttaaac 2760
aagtatttgt taattttagaa aactttaaag cgtttgcaca gatcaactta ccaggcacca 2820
aaagaagtaa aagcaaaaaaa gaaaaccttt cttcaccaaa tcttgggtga tgccaaaaaa 2880
aaatacatgc taagagaagt agaaatcata gctggttcac actgaccaag atacttaagt 2940
gctgcaattg cacgcggagt gagttttta gtgcgtgcag atggtgagag ataagatcta 3000
tagcctctgc agcggaatct gttcacaccc aacttggtt tgctacataa ttatccagga 3060
agggaataag gtacaagaag cattttgtaa gttgaagcaa atcgaatgaa attaactggg 3120

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taatgaaaca aagagttcaa gaaataagtt tttgtttcac agcctataac cagacacata 3180
ctcattttc atgataatga acagaacata gacagaagaa acaaggttt cagtcacccac 3240
agataactga aaatttattta aaccgctaaa agaaacttac tttctcacta aatctttat 3300
aggatttattt taaaatagca aaagaagaag tttcatcatt ttttacttcc tctctgagtg 3360
gactggcctc aaagcaagca ttcagaagaa aaagaagcaa cctcagtaat ttagaaatca 3420
tttgcaatc ccttaatatc ctaaacatca ttcatttttgc ttgttgggt tggttggtag 3480
acagagtctc gctctgtcgc caggctagag tgcggggcg cgatcttgc tcactgcaat 3540
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catgttggcc aggttgtct cgagtctcct gacctcgtga tccacccgac tcggcctccc 3720
aaagtgctgg gattacaggt gtaagccacc gtgccagcc ctaaacatca ttcttgagag 3780
cattgggata ttcctgaaa aggttatga aaaagaagaa tctcatctca gtgaagaata 3840
cttctcattt tttaaaaaag cttaaaactt tgaagttgc tttaacttaa atagtatttc 3900
ccatttatcg cagacctttt ttaggaagca agcttaatgg ctgataattt taaattctct 3960
ctcttgagg aaggactatg aaaagctaga attgagtgtt taaagttcaa catgttattt 4020
gtaatagatg tttgatagat tttctgctac tttgctgcta tggtttctc caagagctac 4080
ataatttatgt ttcatataaa gtatcatcag tgtagaacct aattcaattc aaagctgtgt 4140
gtttggaaga ctatcttact attcacaac agcctgacaa catttctata gccaaaaata 4200
gctaaataacc tcaatcagtc tcagaatgtc atttggtaac tttggggcc acataagcca 4260
ttattcacta gtatgactag ttgtgtctgg cagtttatat ttaactctct ttatgtctgt 4320

23546-08072/US (BIOLO002US)

ggatttttc cttcaaagtt taataaattt atttcttgg attcctgata atgtgcttct 4380

gttatcaaac accaacataa aaatgatcta aacc 4414

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 5

gatgtcccaa tgtgacatgc a 21

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 6

aagtaggcat tgtccataag gaagtt 26

<210> 7

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Probe

<400> 7

ccggaaatgg tctcaactctg ccaaga

26

<210> 8

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 8

gaagggtgaag gtcggagtc

19

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 9

gaagatggtg atgggatttc

20

<210> 10

<211> 20

<212> DNA

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<220>

<223> PCR Probe

<400> 10

caagcttccc gttctcagcc

20

<210> 11

<211> 4174

<212> DNA

<213> M. musculus

<220>

<221> unsure

<222> 2636

<223> unknown

<221> unsure

<222> 2666

<223> unknown

<221> unsure

<222> 2759

<223> unknown

<221> unsure

<222> 2789

<223> unknown

<221> unsure

<222> 3326

<223> unknown

<221> unsure

<222> 3352

<223> unknown

<221> unsure

<222> 3503

<223> unknown

<221> unsure

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<222> 3668

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<222> (240)...(2192)

<400> 11

tgacaaccca cgagctgcc a g c a g g c g c a g c c a t g g g a a g a g g a g g c g g t c a g g a g g a g c 60

g g c g g c a c t g g c a g g c g g c t g c t a c a g c g c g g t g g t g g c g a c g g c t g t t a c t g a a c c 120

c c g g c a g c c g c g g g a t c c c g g c t g c a c g c g g c t g g a g g c c t c g g c t c a g c a g c 180

c c c c a a g c g g a c a c g a a c c c g c t t c t g t c t c c c g a g g c g a a a c t c c g a g g t g c t c a g g t 239

a t g g a t c t t g t c a g g t c t t c t a c c t t g g a c t g c a g c t g g a c c a g c 287

M e t A s p L e u C y s G l n V a l P h e L e u T h r L e u A l a L e u A l a V a l T h r S e r

1

5

10

15

a g c a c a t t t t c t g g a a g t g a g g t c a c a c c a g c t a c t c t t g g c a a a g c t 335

S e r T h r P h e S e r G l y S e r G l u A l a T h r P r o A l a T h r L e u G l y L y s A l a

20

25

30

t c c c c a a g t c t g g a a g a a t c a a t c c a a g c c t g g g a c a a g t t c t t c t 383

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Ser Pro Val Leu Gln Arg Ile Asn Pro Ser Leu Gly Thr Ser Ser Ser

35

40

45

gga aag cct cga ttc acc aag tgt cgt tcc cct gaa ctg gag aca ttt 431
 Gly Lys Pro Arg Phe Thr Lys Cys Arg Ser Pro Glu Leu Glu Thr Phe
 50 55 60

tca tgc tac tgg aca gaa gga gat aat cct gat tta aag acc cca gga 479
 Ser Cys Tyr Trp Thr Glu Gly Asp Asn Pro Asp Leu Lys Thr Pro Gly
 65 70 75 80

tct att cag ctg tac tat gct aaa agg gaa agc caa cga caa gct gca 527
 Ser Ile Gln Leu Tyr Tyr Ala Lys Arg Glu Ser Gln Arg Gln Ala Ala
 85 90 95

aga att gct cat gaa tgg acc cag gaa tgg aaa gaa tgc cct gat tat 575
 Arg Ile Ala His Glu Trp Thr Gln Glu Trp Lys Glu Cys Pro Asp Tyr
 100 105 110

gtc tct gct gga aaa aac agc tgt tac ttc aac tca tca tat acc tcc 623
 Val Ser Ala Gly Lys Asn Ser Cys Tyr Phe Asn Ser Ser Tyr Thr Ser
 115 120 125

att tgg ata ccc tac tgc atc aag cta act aca aat ggt gat ttg ctg 671
 Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Thr Asn Gly Asp Leu Leu
 130 135 140

gac caa aaa tgt ttc act gtt gac gaa ata gtg caa cct gat cca ccc 719
 Asp Gln Lys Cys Phe Thr Val Asp Glu Ile Val Gln Pro Asp Pro Pro
 145 150 155 160

att ggc ctc aac tgg act tta cta aac att agt ttg acc ggg att cgt 767
 Ile Gly Leu Asn Trp Thr Leu Leu Asn Ile Ser Leu Thr Gly Ile Arg
 165 170 175

gga gac atc caa gtg agt tgg caa cca cca ccc aat gca gat gtt ctg 815
 Gly Asp Ile Gln Val Ser Trp Gln Pro Pro Pro Asn Ala Asp Val Leu
 180 185 190

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aag gga tgg ata att ctg gag tat gaa att cag tac aaa gaa gta aat 863
 Lys Gly Trp Ile Ile Leu Glu Tyr Glu Ile Gln Tyr Lys Glu Val Asn
 195 200 205

gaa tca aaa tgg aaa gtg atg ggc cct ata tgg tta aca tac tgt cca 911
 Glu Ser Lys Trp Lys Val Met Gly Pro Ile Trp Leu Thr Tyr Cys Pro
 210 215 220

gtg tac tca ttg aga atg gat aaa gaa cat gaa gtg cgg gtg aga tcc 959
 Val Tyr Ser Leu Arg Met Asp Lys Glu His Glu Val Arg Val Arg Ser
 225 230 235 240

aga caa cgg agc ttt gaa aag tac agc gag ttc agc gaa gtc ttc cgt 1007
 Arg Gln Arg Ser Phe Glu Lys Tyr Ser Glu Phe Ser Glu Val Leu Arg
 245 250 255

gta ata ttt cct cag acg aac ata ttg gaa gca tgt gaa gaa gat atc 1055
 Val Ile Phe Pro Gln Thr Asn Ile Leu Glu Ala Cys Glu Glu Asp Ile
 260 265 270

cag ttt cca tgg ttc tta att att atc ttt gga ata ttt gga gta gca 1103
 Gln Phe Pro Trp Phe Leu Ile Ile Phe Gly Ile Phe Gly Val Ala
 275 280 285

gtg atg cta ttt gta gtt ata ttt tca aag cag caa agg att aag atg 1151
 Val Met Leu Phe Val Val Ile Phe Ser Lys Gln Gln Arg Ile Lys Met
 290 295 300

ctg att tta ccc cca gtc cca gtt cca aag att aaa ggg att gat cca 1199
 Leu Ile Leu Pro Pro Val Pro Val Pro Lys Ile Lys Gly Ile Asp Pro
 305 310 315 320

gat ctt ctc aag gga ggg aag ttg gag gag gtg aac acc atc tta ggc 1247
 Asp Leu Leu Lys Gly Gly Lys Leu Glu Glu Val Asn Thr Ile Leu Gly
 325 330 335

att cat gat aac tac aaa ccc gac ttc tac aat gat gat tcc tgg gtc 1295
 Ile His Asp Asn Tyr Lys Pro Asp Phe Tyr Asn Asp Asp Ser Trp Val
 340 345 350

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gag ttc att gag cta gat att gat gaa gca gat gtg gat gag aag act 1343
 Glu Phe Ile Glu Leu Asp Ile Asp Glu Ala Asp Val Asp Glu Lys Thr
 355 360 365

gaa ggg tct gac aca gac aga ctt cta agc aat gat cat gag aaa tca 1391
 Glu Gly Ser Asp Thr Asp Arg Leu Leu Ser Asn Asp His Glu Lys Ser
 370 375 380

gct ggt atc ctt gga gca aag gat gat tct ggg cgt acc agc tgt 1439
 Ala Gly Ile Leu Gly Ala Lys Asp Asp Asp Ser Gly Arg Thr Ser Cys
 385 390 395 400

tac gac cct gac att ttg gat act gat ttc cat acc agt gac atg tgt 1487
 Tyr Asp Pro Asp Ile Leu Asp Thr Asp Phe His Thr Ser Asp Met Cys
 405 410 415

gat ggt acc ttg aag ttt gct cag tca cag aag tta aat atg gaa gct 1535
 Asp Gly Thr Leu Lys Phe Ala Gln Ser Gln Lys Leu Asn Met Glu Ala
 420 425 430

gat ctc ttg tgc ctt gat cag aag aat ctg aag aac ttg cct tat gat 1583
 Asp Leu Leu Cys Leu Asp Gln Lys Asn Leu Lys Asn Leu Pro Tyr Asp
 435 440 445

gct tcc ctt ggc tct ctg cat ccc tcc att acc cag aca gta gaa gaa 1631
 Ala Ser Leu Gly Ser Leu His Pro Ser Ile Thr Gln Thr Val Glu Glu
 450 455 460

aac aag cca cag cca ctt ttg agc agc gaa act gag gca acc cac caa 1679
 Asn Lys Pro Gln Pro Leu Leu Ser Ser Glu Thr Glu Ala Thr His Gln
 465 470 475 480

ctc gcc tct aca ccg atg agt aat ccc aca tca ctg gca aac att gac 1727
 Leu Ala Ser Thr Pro Met Ser Asn Pro Thr Ser Leu Ala Asn Ile Asp
 485 490 495

ttt tat gcc caa gta agc gac att aca cca gca ggt ggt gat gtc ctt 1775
 Phe Tyr Ala Gln Val Ser Asp Ile Thr Pro Ala Gly Gly Asp Val Leu

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500

505

510

tcc cca ggc caa aag att aag gca ggg ata gcc caa ggc aat acc cag 1823
Ser Pro Gly Gln Lys Ile Lys Ala Gly Ile Ala Gln Gly Asn Thr Gln

515

520

525

cgg gag gtg gcc acg ccc tgc caa gaa aat tac agc atg aac agt gcc 1871
Arg Glu Val Ala Thr Pro Cys Gln Glu Asn Tyr Ser Met Asn Ser Ala
530 535 540

tac ttt tgt gag tca gat gcc aaa aaa tgc atc gct gtg gcc cgt cgc 1919
Tyr Phe Cys Glu Ser Asp Ala Lys Lys Cys Ile Ala Val Ala Arg Arg
545 550 555 560

atg gaa gcc acg tct tgt ata aaa cca agc ttt aac caa gag gac att 1967
Met Glu Ala Thr Ser Cys Ile Lys Pro Ser Phe Asn Gln Glu Asp Ile
565 570 575

tac atc acc aca gaa agc ctt acc act act gcc cag atg tct gag aca 2015
Tyr Ile Thr Thr Glu Ser Leu Thr Thr Ala Gln Met Ser Glu Thr
580 585 590

gca gat att gct cca gat gct gag atg tct gtc cca gac tac acc acg 2063
Ala Asp Ile Ala Pro Asp Ala Glu Met Ser Val Pro Asp Tyr Thr Thr
595 600 605

gtt cac acc gtg cag tct cca agg ggc ctt ata ctc aac gca act gct 2111
Val His Thr Val Gln Ser Pro Arg Gly Leu Ile Leu Asn Ala Thr Ala
610 615 620

ttg cct ttg cct gac aaa aag aat ttt ccc tcc tcg tgt ggt tat gtg 2159
Leu Pro Leu Pro Asp Lys Lys Asn Phe Pro Ser Ser Cys Gly Tyr Val
625 630 635 640

agc aca gac caa ctg aac aaa atc atg cag tag ctttcctat cttaaatgg 2212
Ser Thr Asp Gln Leu Asn Lys Ile Met Gln
645 650

caagggaaag gctgggcaca aacgcttaaa ccaaaaactat gtttaaatc tgtgttggga 2272

gagcatgaga gtggatatgg attctaaaat acttttctg gaaatgtcaa aatatcaata 2332
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23546-08072/US (BIOLO002US)

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23546-08072/US (BIOLO002US)

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23546-08072/US (BIOLO002US)

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acatcattct tgagagcatt

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23546-08072/US (BIOLO002US)

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23546-08072/US (BIOLO002US)

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23546-08072/US (BIOLO002US)

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23546-08072/US (BIOLO002US)

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aaattacagc atgaacagtg

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23546-08072/US (BIOLO002US)

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23546-08072/US (BIOLO002US)

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ttggatatgc aaaacattta

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aaactccgag gtactggagg

20

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tgctaacctg gagcaaggac

20

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23546-08072/US (BIOLO002US)

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gagtcgggtc acgtctggag

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aagctgcaag gtttgtgaag

20

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agagagctac ctaactaaca

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23546-08072/US (BIOL0002US)

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02/26/04